

AP Biology

Unit 1 – Evolution

Notes & Practice Exam

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SECTION 1 - MECHANISMS OF EVOLUTION

1.1 – WHAT IS THE SCIENTIFIC MEANING OF EVOLUTION & THE 5 MAIN MECHANISMS OF EVOLUTION?

Evolution can be misunderstood based on the many ways people think it is defined. In this course **evolution** is defined as a change in the genetic makeup of a population over generations. The genetic makeup of a population refers to the various **alleles** coding for traits of all types. For example, plant height is a trait with two alleles, tall and short. In all populations, there will be a certain frequency of recessive alleles and dominant alleles. Any mechanism that shifts the frequencies of alleles is a mechanism of evolution. The 5 main mechanisms that cause allele frequencies to shift are **Natural Selection, Genetic Drift, Gene Flow, Preferential Mating, & Mutations**. The next sections will discuss each of these 5 mechanisms in detail.

1.2 – HOW DO MUTATIONS & GENE FLOW CAUSE EVOLUTION?

Imagine a scientist has been observing a population of brown (grizzly) bears for 5 years. One day a pure white cub emerges from a den with its brown mother and siblings. No white grizzly bears have ever been documented before this event. What caused the white bear to suddenly appear? There is no magic in science, so the only explanation is a mutation in the fur gene. A **mutation** is a change in DNA, RNA or amino acid sequence. When mutations cause the physical result of a gene to change, this leads to variation among the members in a population. Mutations are random and increase or decrease the frequencies of alleles randomly.

In a different scenario imagine 2 islands very close to each other. One island has only red parrots and the other has only green parrots. One day a red parrot is seen on the green parrot island. Again, no magic here...just a mutation or a migration of organisms and their alleles. **Gene flow** is the proper term for movement of individuals into or out of a population (migrations). After the migration, the green parrot island now has a member that is red; therefore, the red allele has increased in the population and the green allele has decreased.

1.3 – HOW DOES GENETIC DRIFT CAUSE EVOLUTION?

At the molecule level mutations occur simply by chance (most times) but sometimes entire organisms also survive better than others *simply by chance*. Imagine an ant collecting food for its colony and happens to be the strongest & most reproductively healthy...oops I just stepped on it! **Genetic drift** is an unpredictable change in allele frequencies. If the ant colony only had 10 ants in it and the one I stepped on was the only brown ant, then the frequency of the other color, say red, is the only color remaining. 1/10 ants is 10% of that ant population but if the population is larger, say 1 million, then 10% is 100,000 ants. If I still just step on one brown ant on my way out the door, it is less probable that I happen to step on the only brown ant in the large population. As a general rule, genetic drift impacts smaller populations much more than larger populations. Genetic drift is always a factor for any population, but larger populations don't change as drastically from a single random chance event.

1.4 – HOW DOES NATURAL SELECTION CAUSE EVOLUTION?

Any feature that allows an organism to survive and therefore have a higher probability of reproducing is called an **adaptation**. Essential to the theory of natural selection is the existence of variation in a population. If all individuals are identical, they would all be equally probable of mating, getting nutrients and leaving offspring identical to them. In most populations there is much diversity among members that give certain individuals higher chances of survival and reproductive success in

their environments, termed survival of the fittest. **Natural selection** is a mechanism of evolution where individuals with adaptations affording them reproductive success and survival will pass on these adaptations to their offspring, causing an increase in those trait's allele frequencies and a decrease in non-advantageous alleles. Why do the non-advantageous alleles decrease? This is due to the individuals possessing them not surviving to reproduce and populate the subsequent generations. Beneficial traits may not always remain beneficial however; if the environment changes then a different set of traits may become more favorable leading to other allele frequencies shifting, and thus, the traits becoming different.

1.5 – WHY IS PREFERENTIAL MATING DIFFERENT FROM NATURAL SELECTION?

Not all adaptations will ensure higher reproductive opportunities. A type of natural selection called **sexual selection (preferential mating)** is when certain traits afford a higher probability of being *selected* by the opposite sex for mating. In many instances some of these traits actually decrease survival rate but increase sexual selection, so this is a very unique type of selection pattern. Bird coloration is an excellent example in which males are brightly colored and vocal, attracting mates but also predators. The females however are usually neutrally colored providing camouflage.

1.6 – WHICH MECHANISMS CAUSE THE GREATEST CHANGES IN POPULATIONS?

Large sexually reproducing populations are affected greatly by sexual selection & natural selection. If the population is small, genetic drift predominates because diversity drops and natural selection will not occur predictably. Mutations always occur but a harmful mutation has a high probability of becoming “locked” or fixed in the population if it is small, due to natural selection not operating: individuals with ill traits could predominate by chance, possibly leading to species extinction. Migrations occur depending on the environment/location and their effects can vary.

Asexual populations change only by mutations, migrations and genetic drift. Because there is no sex, there can be no natural selection! This is referred to as “The cost of sex” in a species. Reproducing sexually requires much energy to find mates, generate offspring and, in many cases, spend years rearing them. The benefits though include the ever important diversity factor that allows for natural selection and a population that can adjust to changing environments. Asexual populations are at the mercy of their environment; if a change occurs that the asexual population cannot survive, they will go extinct. Some of the most successful organisms have mechanisms to reproduce both asexually & sexually; some prokaryotes also have mechanisms to exchange DNA with each other, not truly sexual reproduction, but certainly demonstrates the importance of diversity to survival in our wide world of organisms.

SECTION 2 – THE HARDY-WEINBERG THEORY

2.1 – WHAT IS THE HARDY-WEINBERG THEORY?

The 5 mechanisms of evolution discussed in section 1 can be measured and detected in almost any population. We know the mechanisms can cause a shift in allele frequencies, so what about if we use that to state the **null hypothesis**: There will be no change in allele frequencies from one generation to the next if the 5 mechanisms of evolution are NOT occurring. If we assume this is the case, the allele frequencies would stay the same forever and we can use 2 formulas to calculate what those frequencies of alleles are; this is known as the **Hardy-Weinberg Theory**. In reality, evolution does occur and if we know some information about the population, we can figure out which mechanism(s) are causing the allele frequencies to change.

2.2 – WHAT ARE THE PARTS OF THE HARDY-WEINBERG EQUATIONS?

The first equation is $p + q = 1$, where **p = the frequency of the dominant allele** & **q = the frequency of the recessive allele**. If you know that the frequency of the recessive allele is 20% (.20) then the frequency of the dominant allele must be 80% (.80) so that both allele frequencies sum to 100% (1).

The second equation is $p^2 + 2pq + q^2 = 1$, where **p² = the frequency of the homozygous dominant genotype**, **2pq = the frequency of the heterozygous genotype** and **q² = the frequency of the homozygous recessive genotype**. Remember that a **genotype** is the 2-allele combination such as GG, Gg or gg. Instead of a single letter, the letters p & q are used to make the 3 possible genotype combinations. An example is if there are 20% of individuals homozygous recessive (q²) for a trait, then the remaining 80% will be some homozygous dominant (p²) and some heterozygous (2pq).

2.3 HOW ARE THE HARDY-WEINBERG EQUATIONS USED?

In order to calculate frequencies of **genotypes** we must know the frequencies of the alleles that make up the genotypes. If .36 of a population is homozygous recessive (q²), we can calculate the frequency of the recessive allele by taking the square root of q², which gives .60 as q. Remember that a homozygous recessive individual has 2 recessive alleles and so will only appear like the recessive form of the trait. The equation $p + q = 1$ can now be used to solve for p: $p + .60 = 1$, gives **p = .40**. Now we know the values of p & q and can substitute them into the other equation, $p^2 + 2pq + q^2 = 1$. q² is already known to be .36, so the $p^2 + 2pq$ values must sum to .64 and this represents the frequency of the dominant **phenotype** according to the law of dominance. However, the frequency of homozygous dominant individuals have 2 dominant alleles and is p² or .40² = .16, whereas the frequency of heterozygous individuals have 1 dominant allele and 1 recessive allele and is 2pq or [2 x (.40) x (.60)] = .48. A step by step equation model is shown below:

Step 1	$p + q = 1$	$p^2 + 2pq + q^2 = 1$	Set up equations side by side
Step 2	$p + q = 1$	$p^2 + 2pq + .36 = 1$	Know that .36 is q ² , hom. rec. genotype
Step 3	$p + .6 = 1$	$p^2 + 2pq + .36 = 1$	Square root q ² to get q recessive allele
Step 4	$.4 + .6 = 1$	$p^2 + 2pq + .36 = 1$	Find p dominant allele based on q
Step 5	$.4 + .6 = 1$	$.16 + 2pq + .36 = 1$	Find p ² hom. dom genotype based on p
Step 6	$.4 + .6 = 1$	$.16 + .48 + .36 = 1$	Find 2pq hetero. genotype based on p & q

SECTION 3 – EVIDENCE OF UNITY & DIVERSITY OF LIFE

3.1 – WHAT MOLECULAR EVIDENCE DEMONSTRATES UNITY & DIVERSITY?

All life shares common **biomolecules** like **DNA** that has the same **nucleotide** building blocks but their sequences and thus genes & phenotypes vary among individuals. Plants and algae have **cellulose** as cell wall **carbohydrates**, animals have **adipose** to store fats for energy sources, and all life shares **phospholipids** & **proteins** as cell membrane foundations. The diversity arises based on the specific sequences of molecules such as membrane proteins having similar but not identical gene sequences. These molecule examples all show that life has common biomolecules but over time different species have evolved in distinct conditions and the underlying molecules have adjusted in those conditions.

3.2 – WHAT CELLULAR EVIDENCE DEMONSTRATES UNITY & DIVERSITY?

All cells have 4 basic parts needed for life processes. The **plasma membrane** surrounds the cell and regulates how materials move in and out of the cell. Within the cell the **cytoplasm** is the liquid inside the cell. **DNA** provides instructions to direct the cells processes & code for traits. Finally, all cells need proteins that are produced by parts called **ribosomes**. Diversity among life can be seen at the cell level based on cell complexity. **Eukaryotes** have the 4 basic cell parts above but also specialized **organelles** used for specific tasks. **Prokaryotes** lack these specialized organelles meaning they can be smaller and are much less complex. Evidence of their close relationship will be discussed in section 5.2.

3.3 – WHAT MECHANISTIC EVIDENCE DEMONSTRATES UNITY & DIVERSITY?

Some mechanisms and processes elucidate our common ancestry such as **glycolysis**. This process breaks down **glucose** to make some **ATP** and occurs in the absence of oxygen. All life uses glycolysis and the enzymes from eukaryote cells and prokaryote cells are very similar. Eukaryotes also have the ability to continue the metabolism of glucose further during **cellular respiration** in the **mitochondria** using oxygen but prokaryotes lack mitochondria; however, many prokaryotes still use cell respiration but the enzymes usually in our mitochondria are on their cell membranes instead. A similar situation exists for the process of **photosynthesis**: specialized **chloroplasts** contain pigments & enzymes in eukaryotes but these enzymes & pigments are on the cell membrane of photosynthetic prokaryotes instead of inside chloroplast membranes.

3.4 – WHAT ANATOMICAL EVIDENCE DEMONSTRATES UNITY & DIVERSITY?

In multicellular organisms there are many similarities that reflect common ancestry. A classic example is embryo development in vertebrate animals. We all share a nearly identical appearance in early development including a tail. As development progresses, our unique DNA then codes for our vastly different appearances such as shell formation in turtles and finger formation in primates. Structures that reflect this shared DNA are called **homologous structures**. Other structures that are just the result of adaptations in similar environments are called **analogous structures**, such as wings of bats & birds.

3.5 – HOW DO PHYLOGENETIC TREES MODEL UNITY & DIVERSITY

A **phylogenetic tree** is a diagram that shows descent with modification using DNA or amino acid sequences. Phylogenetic trees appear as branched tree-like diagrams with similar groups closer to each other and more distant groups further from each other. Whatever method is used to construct trees, most are based on genetic changes and therefore represent an organism's **phylogeny**, a model of an organism's evolutionary history. Closely related organisms will share more similar traits & thus DNA; as DNA changes over time, populations diverge and create 'branches' on phylogenetic trees.

SECTION 4 – MECHANISMS OF SPECIATION

4.1 – WHAT IS SPECIATION & HOW IS IT DEFINED DIFFERENTLY?

Speciation is the process in which new populations arise by diverging genetically from existing populations. The definition can also be adjusted according to the population's reproduction mechanism. Asexual populations do not diverge based on reproductive mechanisms, rather only by random mutations & some other unique forms of genetic exchange you will study in future units. Sexual populations have mutations to change their genetics randomly but also undergo sexual reproduction which introduces a multitude of genetic change mechanisms. **Biological speciation** is strictly used to define a mechanism that prevents breeding between populations and then the 5 mechanisms of evolution can occur & further the speciation process until the 2 populations can no longer reproduce together successfully.

4.2 – HOW DO POPULATIONS BECOME REPRODUCTIVELY ISOLATED?

The first type of speciation is called **allopatric speciation** in which populations become reproductively isolated by physical barriers like canyons, bodies of water or even highways. As time passes the 5 mechanisms of evolution will cause these 2 isolated populations to evolve differently from each other, ultimately leading to their inability to reproduce & produce fertile offspring. The second type of speciation is called **sympatric speciation** in which populations become reproductively isolated while living in the same area. Some mechanism will cause a population to stop breeding and then the 5 mechanisms of evolution will cause them to become distinct species over time. A very interesting example is **polyploidy** in which cell division errors lead to extra chromosome sets in offspring. Although usually lethal in animals, this phenomenon is quite common in plants and produces very hardy crops such as wheat.

4.3 – HOW DOES REPRODUCTIVE ISOLATION OCCUR?

A reproductive barrier can occur before a zygote is formed, called **prezygotic barriers**, or after a zygote has formed, called **postzygotic barriers**. The 5 prezygotic barriers are **Habitat Isolation**, **Temporal Isolation**, **Behavioral Isolation**, **Mechanical Isolation** and **Gametic Isolation**. The 3 postzygotic barriers are **Reduced Hybrid Viability**, **Reduced Hybrid Fertility** and **Hybrid Breakdown**. In your note outlines be sure to read & list the textbook examples of each mechanism. You should analyze each barrier and determine its role in both allopatric & sympatric speciation.

4.4 – HOW QUICKLY DOES SPECIATION TAKE PLACE?

The rate of speciation is determined by the species, the mechanisms causing it and the environmental conditions. During times of intense environmental change evidenced in the fossil record, speciation has occurred within a few generations while in other cases it took hundreds of years. Organisms with fast life cycles like insects and bacteria tend to evolve more rapidly than slow breeding organisms like mammals. Environmental pressures will favor individuals with the best adaptations for survival and this may not always be a single phenotype, meaning two or more subpopulations may be equally capable of surviving and will continue to produce offspring with those traits, leading to distinct species.

SECTION 5 – THEORIES OF LIFE’S ORIGIN & EVOLUTION ON EARTH

5.1 – WHEN DID LIFE ARISE?

According to fossil & other geologic evidence, the Earth formed about 4.6 billion years ago (bya) and was a very hostile environment with extreme temperatures, UV radiation, toxic levels of gases like methane & sulfur dioxide and carbon dioxide. Small organic molecules could certainly form but their aggregation into a complex system was not evidenced until 3.5 bya, meaning cells took over a billion years to form from basic biomolecules. Essential to life was a molecule to store & transmit genetic information. In the **RNA-World Hypothesis**, conditions were too hostile for the delicate DNA molecule, so it is thought that RNA was actually the first genetic molecule instead of DNA since it is diverse in form, catalytic, self-replicating and carries genetic information.

5.2 – WHAT WERE SOME ESSENTIAL EVENTS LEADING TO MULTICELLULARITY?

Once RNA had been established inside of cells, the DNA molecule could then evolve as the permanent genetic code. The early Earth did not have much oxygen so all metabolism required **glycolysis** to break down sugars for ATP in the absence of oxygen. About 2.6 bya a steady increase in the amount of atmospheric oxygen occurred as evidenced by large rock bands of iron oxide (rust) that result from the reaction of oxygen & solid iron. Alongside this oxygen revolution are fossils of photosynthetic prokaryotes, leading to the conclusion that this was the evolutionary timeframe of photosynthesis evolving. Ancient types of photosynthesis probably used pigments that absorbed UV light since that was still prominent on the planet but as Earth evolved, so did the pigment types. As oxygen accumulated in the atmosphere as a product of photosynthesis, many **anaerobic** organisms went extinct or found anaerobic habitats but those that could evolve **aerobic** respiration would flourish.

Multicellular organisms likely arose based on the **endosymbiont theory** which asserts that multiple prokaryotes formed a **symbiotic** relationship and ultimately formed a colonial group of cells, later becoming a united cell with **organelles** being the remnants of the early prokaryote symbionts. Each prokaryote provided some specialized role such as **photosynthetic** prokaryotes becoming **chloroplasts** and **heterotrophic** prokaryotes becoming **mitochondria**.

5.3 – WHAT PATTERNS ARE FOUND IN THE TIMELINE OF LIFE?

Life has flourished on this planet but it has also nearly perished several times. **Mass extinctions** have occurred numerous times and are usually associated with some major geologic event that destroys large masses of species. For example the Cretaceous extinction wiped out the dinosaurs and many other species while the Permian extinction saw the loss of 96% of marine species. While the theories on what exactly caused the mass extinctions are not completely agreed upon, the pattern of what happened afterwards is clear. As mass quantities of species are wiped out, the environment becomes a fresh start for surviving organisms. Mammals are a striking example of a now unbelievably diverse group that would likely have remained only small rodents if the dinosaurs never went extinct since they would be preyed upon constantly. This diversification of organisms after extinctions or other habitat-opening events is called **adaptive radiation**.

AP Biology - Unit 1 Exam Practice

These practice questions were used on previous year's exam. While the level of question difficulty and format will be similar, the questions will not be the same; so be sure to understand all the notes & lab topics even if not shown here.

Questions 1 - 3

An investigation was conducted on the critically endangered stream-breeding mountain newt, *Neurergus kaiseri*, within its entire range in southwestern Iran. Two distinct populations were studied: Northern populations, located in more humid habitats at higher elevation, and Southern populations, from drier habitats at lower elevation. The investigation concluded that the 2 populations demonstrate high levels of divergence from each other but can still mate together. However, these matings do not result in any viable offspring.

1. According to the study, which of the following is the most likely cause of the newt populations' evolution?
 - a. The large populations are subjecting them to increased genetic drift.
 - b. The increased activities of humans in the region are disrupting the newt's breeding cycles.
 - c. Members of the original population had some selective advantage in their current habitats.
 - d. The population members became isolated due to polyploidy occurring in certain individuals.
2. Among the 2 newt populations which mechanism is driving their genetic divergence?
 - a. Temporal Isolation
 - b. Gametic Isolation
 - c. Mechanical Isolation
 - d. Habitat Isolation
3. Scientists are interested in conserving this species as they play a fundamental role in their ecosystems. Which of the following would be the best course of action for re-developing a healthy population?
 - a. Bring in the same newt species from similar habitats to help increase population sizes in each region.
 - b. Introduce new predators to promote survival of the fittest.
 - c. Transfer the low elevation population to the southern population region.
 - d. Remove half the population from each region, breed in captivity, and release the new population back into the wild population.

Questions 4-5

The three-spined stickleback (*Gasterosteus aculeatus*) is a small fish found in both marine and freshwater environments. Marine stickleback populations consist mainly of individuals with armor-like plates covering most of their body surface (completely plated). Approximately 10,000 years ago, some marine sticklebacks colonized freshwater environments. After many generations in the freshwater environments, the freshwater stickleback populations lacked the armor plating (low plated) typical of marine stickleback populations.

Over the period between 1957 and 2005, one freshwater population, in Lake Washington, a lake in a coastal region of the northwestern United States, changed from having a majority of individuals of the low-plated phenotype to having more individuals of the completely-plated phenotype than of the low-plated phenotype. Figure 1 shows the distribution of plated phenotypes in Lake Washington sticklebacks at four time points between 1957 and 2005.

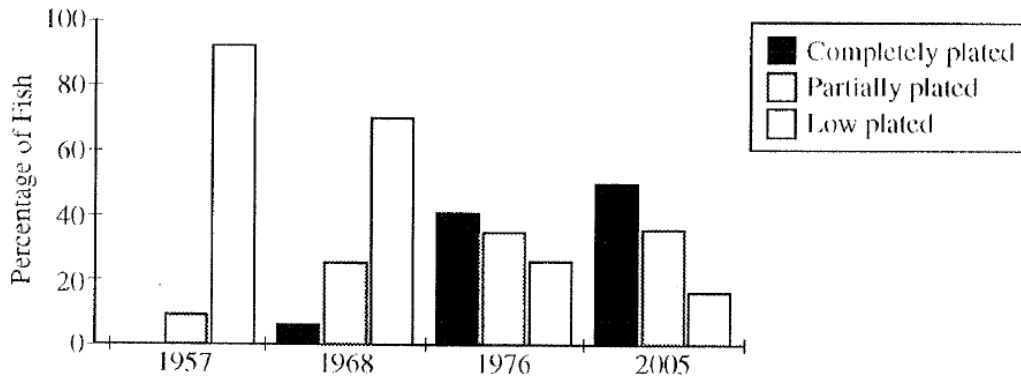


Figure 1. Armor plating phenotypes in Lake Washington stickleback population

A single gene, *ectodysplasin* (*EDA*), is thought to be responsible for the variation in the number of armor plates in sticklebacks. Figure 2 shows a phylogenetic tree constructed by comparing DNA sequences of the *EDA* gene from a number of stickleback populations with low-plated or completely plated phenotypes. Figure 3 shows a phylogenetic tree constructed by comparing the sequences of 25 genes that were randomly selected from the same populations as shown in Figure 2. In both figures, shaded populations display the completely plated phenotype.

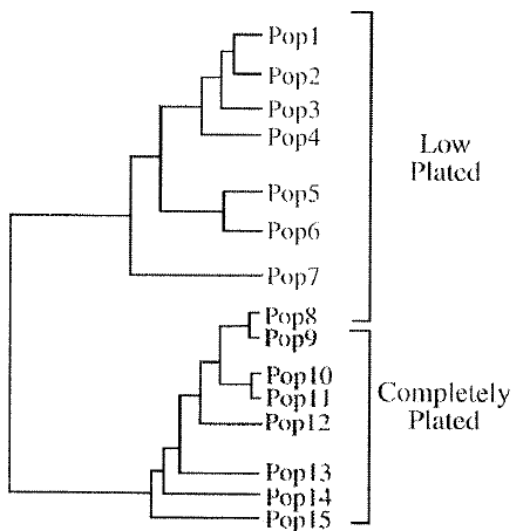


Figure 2. Phylogeny based on *EDA* gene only

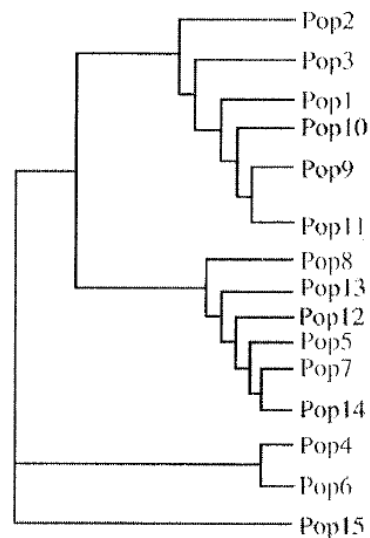


Figure 3. Phylogeny based on 25 random genes

4. Evolution of a new trait typically takes many generations. Yet a dramatic shift in the extent of armor plating in the Lake Washington stickleback population occurred in the 50 years following the lake cleanup. Which of the following best describes the mechanism of the rapid evolution of the armor phenotype in the Lake Washington sticklebacks?
- Pollutants in the lake forced the sticklebacks to increase their mutation rate.
 - The rapid change in the Lake Washington ecosystem required individuals to evolve complete armor plating quickly.
 - The increase in visibility in Lake Washington allowed sticklebacks to visually select mates with low armor.
 - New selective pressures favored individuals with the plated phenotype, causing the plated allele frequency in the population to increase quickly.
5. The phylogenetic trees in Figures 2 and 3 depict two different phylogenies of the same populations of sticklebacks. Which of the following questions will best help determine which tree represents the most accurate phylogeny?
- Is the EDA gene as representative of the differences between the populations as the 25 random genes that were examined for figure 3?
 - Are the low-plated populations found only in freshwater and the high-plated populations found only in saltwater environments?
 - Is the common ancestor of the organisms represented in Figure 2 different from the common ancestor of the organisms represented in Figure 3?
 - Is the expression level of the EDA gene analyzed in Figure 2 significantly greater than the expression levels of the 25 genes analyzed in Figure 3?

Questions 6-7

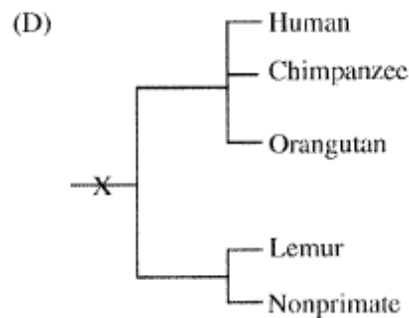
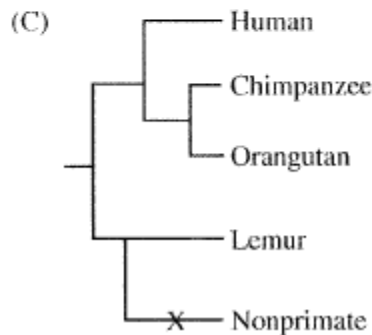
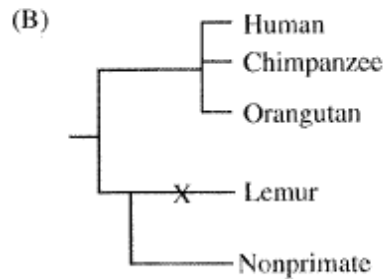
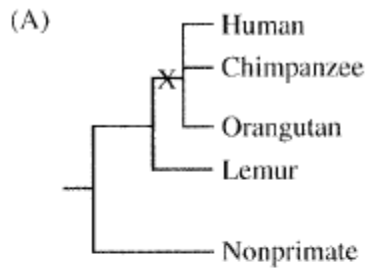
Ascorbic acid is a necessary biomolecule in organism metabolism. Most animals can synthesize this compound but some groups must consume foods containing it to substitute their inability to produce it. The table below identifies groups of animals by their ability to synthesize ascorbic acid.

TABLE I: SELECTED MAMMALIAN GROUPS

Group	Selected Members	Biosynthesis of Ascorbic Acid
Nonprimate mammals	Elephant, mouse	Yes
Primate mammals	Lemur	Yes
	Orangutan, chimpanzee	No
	Human	No

6. The mammals in Table 1 along with 30 random strains of bacteria, 3 random strains of fungi and most species of invertebrates contain a gene for an enzyme that breaks down ascorbic acid. Which of the following is most consistent with this data in terms of the organisms' evolution?
- Biomolecular data is an unreliable source for determining organism relatedness.
 - The requirements for energy & materials reflects how organisms evolve unique solutions to match their unique habitats.
 - Despite differences today, all organisms demonstrate common ancestry.
 - Over a long evolutionary history, this gene must have mutated under selective pressures to become widely different in these organisms.

7. Which of the following phylogenetic trees best demonstrates (with the X) the point at which the mutation causing an inability to synthesize ascorbic acid likely occurred?



Questions 8-9

An experiment from 2003 exposed numerous polymers to high UV light to test if this variable could have been a selective force in the formation of genetic information molecules on the early Earth. The experiment showed that nucleic acids with structures similar to those found in cells today (DNA & RNA) were best able to handle the intense UV light.

8. Which of the following is the best conclusion based on this study?
- Only genetic information molecules can undergo evolution.
 - Natural selection is a driving force underlying many different levels in biological systems.
 - The UV light should have been tested at low levels to best model conditions of the early Earth.
 - The high levels of oxygen on early Earth gave rise to the ozone layer, making UV light a poor variable to test.
9. Which of the following questions would be logical for a follow-up study relevant to determining Earth's first genetic material?
- Was there a significant difference in the abilities of amino acids & RNA to handle intense UV light?
 - Was there a significant difference in the abilities of glucose & RNA to handle intense UV light?
 - Was there a significant difference in the abilities of DNA & amino acids to handle intense UV light?
 - Was there a significant difference in the abilities of DNA & RNA to handle intense UV light?

Free Response

1. A species of Brown Bear inhabits northern regions of New York, bordering Canada. Scientists have documented another bear they call the “Spirit Bear” which has white fur but is not a Polar Bear. The Spirit Bear is believed to originally have been a mutant form of the Brown Bear, caused by a mutation in genes for fur color, but is now being considered as its own species based on various scientific findings.
 - a. If we consider them as the same species and assume that the population is in Hardy-Weinberg equilibrium, **calculate** the frequency of heterozygous individuals if 14% of the population has the recessive mutant white fur.
 - b. Assuming that they have become distinct species, **describe** 1 possible isolating mechanism for the original population diverging in the first place and **describe** 3 likely evolution mechanisms that led to their becoming distinct species.
 - c. **Propose** 2 likely sources of data, other than reproductive incompatibility, that could have been used to determine that the Spirit Bear and the Brown Bear are distinct species.

2.

A research team has genetically engineered a strain of fruit flies to eliminate errors during DNA replication. The team claims that this will eliminate genetic variation in the engineered flies. A second research team claims that eliminating errors during DNA replication will not entirely eliminate genetic variation in the engineered flies.

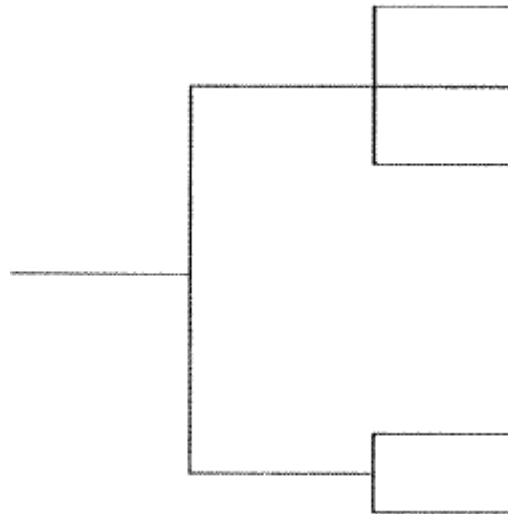
- (a) **Provide** ONE piece of evidence that would indicate new genetic variation has occurred in the engineered flies.
- (b) **Describe** ONE mechanism that could lead to genetic variation in the engineered strain of flies.
- (c) **Describe** how genetic variation in a population contributes to the process of evolution in the population.

3.

MILK COMPONENTS IN DIFFERENT MAMMALS

Character	Cat	Cow	Horse	Human	Pig
Lactose	+	+	+	+	+
Protein A	+	+	+	+	+
Protein B	–	+	+	–	+
Casein	–	+	+	–	+
+ indicates the presence of the character, and – indicates the absence of the character					

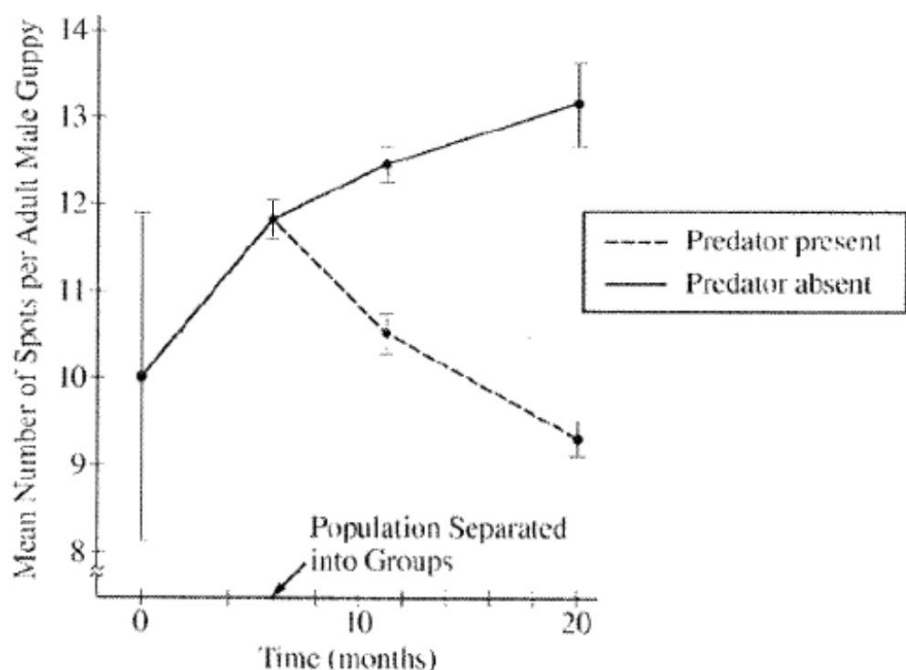
- (a) Using the data in the table, **construct** a cladogram on the template provided to indicate the most likely evolutionary relationships among the different mammals. **Indicate** on the cladogram where each of the characters most likely arose in the evolutionary process, and **justify** the placement of the characters on the cladogram.



4.

Adult male guppies (*Poecilia reticulata*) exhibit genetically determined spots, while juvenile and adult female guppies lack spots. In a study of selection, male and female guppies from genetically diverse populations were collected from different mountain streams and placed together in an isolated environment containing no predators.

The study population was maintained for several generations in the isolated area before being separated into two groups. One group was moved to an artificial pond containing a fish predator, while a second group was moved to an artificial pond containing no predators. The two groups went through several generations in their new environments. At different times during the experiment, the mean number of spots per adult male guppy was determined as shown in the figure below. Vertical bars in the figure represent two standard errors of the mean (SEM).



- Describe the change in genetic variation in the population between 0 and 6 months and **provide** reasoning for your description based on the means and SEM.
- Propose** ONE type of mating behavior that could have resulted in the observed change in the number of spots per adult male guppy between 6 and 20 months in the absence of the predator.
- Propose** an evolutionary mechanism that explains the change in average number of spots between 6 and 20 months in the presence of the predator.